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<110> Transmolecular, Inc. GONDA, Matthew A GREENWOOD, John D
<120> Recombinant Expression Vectors for Functional Nav1.9 Sodium Channels
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Lys Phe Asn Lys Thr Ala Tyr Ala Thr Gln Glu Arg Pro Arg Arg Arg

Trp His Met Asp Asn Phe Tyr His Ser Phe Leu Val Val Phe Arg Ile

Leu Cys Gly Glu Trp Ile Glu Asn Met Trp Gly Cys Met Gln Asp Met

Asp Gly Ser Pro Leu Cys Ile Ile Val Phe Val Leu Ile Met Val Ile

Gly Lys Leu Val Val Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser

Phe Ser Asn Glu Glu Lys Asp Gly Ser Leu Glu Gly Glu Thr Arg Lys

Thr Lys Val Gln Leu Ala Leu Asp Arg Phe Arg Arg Ala Phe Ser Phe

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Asn Ser Pro Lys Pro Lys Glu Thr Thr Glu Ser Phe Ala Gly Glu Asn

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	Ile Asn Cys Val	ttc atg gct aca ggg Phe Met Ala Thr Gly 145	_	486
		att gca gag tgt gtc Ile Ala Glu Cys Val 165	Phe Thr Gly	534
		aaa ata ttg gca aga Lys Ile Leu Ala Arg 180		582
		gat cca tgg aac tgg Asp Pro Trp Asn Trp 195		630

att Ile	gtc Val	att Ile	gga Gly	ata Ile 205	gcg Ala	att Ile	gtg Val	tca Ser	tat Tyr 210	att Ile	cca Pro	gga Gly	atc Ile	acc Thr 215	atc Ile	678
					cgt Arg											726
					cgt Arg											774
					gtc Val											822
					gta Val 270											870
					agg Arg											918
	_		_		gaa Glu	_		_								966
					ggt Gly											1014
					aat Asn											1062
					ctt Leu 350											1110
					caa Gln											1158
			Phe		gtg Val											1206
			380													
			ctg		gtt Val											1254

_	_	_		_		_	_		_	_	_	gcc Ala	-			1350
_	_	_						_				ttt Phe				1398
												ttc Phe				1446
												gat Asp 485				1494
												ctg Leu				1542
												ctc Leu				1590
												atg Met				1638
_						_			_		_	aac Asn				1686
_						_	_					tgc Cys 565				1734
												ctg Leu				1782
												gag Glu				1830
												aat Asn				1878
	_				_	_	_	_				att Ile				1926
												gac Asp 645				1974
gct	ctt	ctg	agt	ttt	gca	gat	gta	atg	aac	tgt	gta	ctt	caa	aag	aga	2022

Ala	Leu 650	Leu	Ser	Phe	Ala	Asp 655	Val	Met	Asn	Cys	Val 660	Leu	Gln	Lys	Arg		
					cgt Arg 670											20	070
					act Thr											2	118
					gga Gly											2	166
					gtt Val											22	214
					aaa Lys											22	262
					cac His 750											23	310
					tgc Cys											23	358
					gca Ala											24	406
					gga Gly											24	454
tta Leu	ctg Leu 810	ctc Leu	aat Asn	tcc Ser	ttt Phe	agc Ser 815	aat Asn	gag Glu	gaa Glu	aga Arg	aat Asn 820	gga Gly	aac Asn	tta Leu	gaa Glu	2	502
					act Thr 830											2	550
					gtg Val											2	598
tgg Trp	tgc Cys	agg Arg	aag Lys 860	caa Gln	aac Asn	tta Leu	cca Pro	cag Gln 865	caa Gln	aaa Lys	gag Glu	gtg Val	gca Ala 870	gga Gly	ggc Gly	2	646
					aaa Lys											2	694

875 880 885

					Gln										a cca l Pro	2742
															gcg Ala 920	2790
															g cgc n Arg	2838
atc Ile	aca Thr	caa Gln	cct Pro 940	gag Glu	cct Pro	gaa Glu	caa Gln	cag Gln 945	gcc Ala	tat Tyr	gag Glu	ctc Leu	cat His 950	Glr	g gag n Glu	2886
aac Asn	aag Lys	aag Lys 955	ccc Pro	acg Thr	agc Ser	cag Gln	aga Arg 960	gtt Val	caa Gln	agt Ser	gtg Val	gaa Glu 965	att Ile	gad	atg Met	2934
					Pro										g aag s Lys	2982
															cag 1 Gln 1000	3030
	ggc	ttt														
Asp	Gly			tgg Trp 1005	Leu					. P1		aa aa ys Ly		ln I		3075
gag	aga	Phe tgt	Gly	Trp	Leu aaa Lys	Pro		Met ggt	Val 101	Pi .0 to	co Ly go ti	ys Ly	ys G ca t	ln I gc t ys (Pro 1015 :gt	3120
gag Glu agc	aga Arg	Phe tgt Cys	Gly ttg Leu aag	Trp 1005 ccc Pro 1020	aaa Lys aag	ggo Gly	Glu ttt	Met ggt Gly	Val 101 tgc Cys 102	Price to	go theys Ph	ys Ly	ys G cat co C	ln I gc t ys (ac c sn I	ero 1015 Egt Cys 1030	
gag Glu agc Ser	aga Arg gtg Val	tgt Cys gac Asp	Gly ttg Leu aag Lys	Trp 1005 ccc Pro 1020 aga Arg	aaa Lys aag Lys caa Gln	ggo Gly cct	ttt Phe	ggt ggt Gly tgg	tgc Cys 102 104 104	. Pri	go to	ys Ly tt co ne Pi gg to rp Ti	ys G cat co C gg a rp A	gc tys (care as	ero 1015 egt Cys 1030 etg Leu 1045	3120
gag Glu agc Ser cgg Arg	aga Arg gtg Val aaa Lys	tgt Cys gac Asp acc Thr	Gly ttg Leu aag Lys tgc Cys	Trp 1005 ccc Pro 1020 aga Arg 1035 tac Tyr	aaaa Lys aag Lys caa Gln	ggo Gly cct Pro	c ttt Phe c ccc Pro	ggt ggt ggt tgg Trp	tgc Cys 102 (gtc Val 104 cac His 105	P1.0	gc ttys Phat to the Transfer T	ys Ly tt co ne Pi gg tg rp Ti	ys G ca t co g g a cp A tt g a tg a	In I I I I I I I I I I I I I I I I I I	ero 1015 Egt Cys 1030 Etg Leu 1045 Egc Ser 1060	3120 3165
gag Glu agc Ser cgg Arg ttt Phe	aga Arg gtg Val aaa Lys att Ile	Phe tgt Cys gac Asp acc Thr atc Ile	Gly ttg Leu aag Lys tgc Cys ttt Phe	Trp 1005 ccc Pro 1020 aga Arg 1035 tac Tyr 1050 gtg Val	aaa Lys aag Lys caa Gln att	ggo Gly cct Pro	c ttt Phe C CCC Pro A gto	ggt ggt ggt tgg Trp aaa Lys	tgc Cys 102 (gtc) Val 104 (cac i His 105 (ser 107	Price to	go to	tt cone Progg to Trop Trop Pl	ys G ca C gg a trp A tre G tre a tre	In I I I I I I I I I I I I I I I I I I	ero 1015 gt Cys 1030 etg Leu 1045 agc Ser 1060 ett Phe 1075	3120 3165 3210

				gta Val 1110											3390
				ctt Leu 1125								tct Ser			3435
				tta Leu 1140	_	_	_	_						_	3480
				ctt Leu 1155											3525
		_		gct Ala 1170				_			_		_		3570
_	_		_	tgc Cys 1185						_		_		_	3615
	_			ttt Phe 1200					999 Gly 1205						3660
	_		_	ata Ile 1215								aaa Lys	_		3705
_	_	_		aat Asn 1230						_		-			3750
Cys	Glu	Ser	Gly	Asn	Phe gct	Ser tac	Trp	Ile gct	Asn 1235 ctg	Gln	Lys caa	Val gtg	Asn gca	Phe 1240 aca	3750 3795
Cys gac Asp	Glu aat Asn	Ser gtg Val	Gly gga Gly	Asn 1230 aat Asn	Phe gct Ala gat	ser tac Tyr	Trp ctc Leu	Ile gct Ala tat	Asn 1235 ctg Leu 1250 gca	Gln ctg Leu	Lys caa Gln gtt	Val gtg Val gat	Asn gca Ala tcc	Phe 1240 aca Thr 1255 aca	
Cys gac Asp ttt Phe	Glu aat Asn aag Lys	gtg Val ggc Gly	Gly gga Gly tgg Trp	Asn 1230 aat Asn 1245 atg Met	Phe gct Ala gat Asp	tac Tyr att Ile	Trp ctc Leu ata Ile	gct Ala tat Tyr	Asn 1235 ctg Leu 1250 gca Ala 1265 agc	Gln ctg Leu gct Ala	Lys caa Gln gtt Val tca	Val gtg Val gat Asp	Asn gca Ala tcc Ser	Phe 1240 aca Thr 1255 aca Thr 1270	3795
Cys gac Asp ttt Phe gag Glu att	Glu aat Asn aag Lys aaa Lys	ser gtg Val ggc Gly gaa Glu ttc	Gly gga Gly tgg Trp caa Gln	Asn 1230 aat Asn 1245 atg Met 1260 cag Gln	Phe gct Ala gat Asp cca Pro	tac Tyr att Ile gag Glu atc	Trp ctc Leu ata Ile ttt Phe atc	Ile gct Ala tat Tyr gag Glu ttt	Asn 1235 ctg Leu 1250 gca Ala 1265 agc Ser 1280	Gln ctg Leu gct Ala aat Asn	Lys caa Gln gtt Val tca Ser	Val gtg Val gat Asp ctc Leu ttc	Asn gca Ala tcc Ser ggt Gly act	Phe 1240 aca Thr 1255 aca Thr 1270 tac Tyr 1285 ctg	3795 3840

aaa Lys	aag Lys	tta Leu	ggt Gly	ggc Gly 1320	caa Gln	gac Asp	att Ile	ttt Phe	atg Met 1325	aca Thr	gaa Glu	gaa Glu	cag Gln	aag Lys 1330	4020
				gca Ala 1335											4065
				cgg Arg 1350											4110
				agc Ser 1365									agt Ser		4155
				atg Met 1380											4200
				aaa Lys 1395											4245
	_			acg Thr 1410		_	_						_	_	4290
				ttc Phe 1425								_	_	_	4335
_				tcc Ser 1440		_	_		_				ttg Leu	_	4380
				att Ile 1455											4425
				att Ile 1470											4470
				act Thr 1485											4515
				att Ile 1500											4560
	_		_	ggt Gly 1515	_										4605
tct	gga	atc	gat	gac	ata	ttc	aac	ttc	aag	act	ttt	gcc	agc	agc	4650

Ser	Gly	Ile	Asp	Asp 1530	Ile	Phe	Asn	Phe	Lys 1535	Thr	Phe	Ala	Ser	Ser 1540	
									tca Ser 1550						4695
									gaa Glu 1565						4740
									gcc Ala 1580						4785
									gtt Val 1595						4830
									gcc Ala 1610						4875
									ata Ile 1625						4920
									ttt Phe 1640				tct Ser	_	4965
									gag Glu 1655						5010
									atg Met 1670						5055
_	_	gat Asp	_						att Ile 1685						5100
_		_					_		cta Leu 1700	_			aaa Lys		5145
_	_	_							aat Asn 1715						5190
	_			_				_	aga Arg 1730	_			_	_	5235
	_	gct Ala				_	_		cga Arg	_		_	_	_	5280

1740 1745 1750	
gtg acc aag ggt gac caa ggt gac caa aat gac ttg gaa aac ggg Val Thr Lys Gly Asp Gln Gly Asp Gln Asn Asp Leu Glu Asn Gly 1755 1760 1765	5325
cct cat tca cca ctc cag act ctt tgc aat gga gac ttg tct agc Pro His Ser Pro Leu Gln Thr Leu Cys Asn Gly Asp Leu Ser Ser 1770 1775 1780	5370
ttt ggg gtg gcc aag ggc aag gtc cac tgt gac tgagccctca Phe Gly Val Ala Lys Gly Lys Val His Cys Asp 1785 1790	5413
cctccacgcc tacctcatag cttcacagcc ttgccttcag cctctgagct ccaggggtca	a 5473
gcagcttagt gtatcaacag ggagtggatt caccaaatta gccattccat tttctttct	5533
ggctaaaata aatgatattt caatttcatt ttaaatgata cttacagaga tataagataa	a 5593
ggctacttga caaccagtgg tactattata ataaggaaga agacaccagg aaggactgta	s 5653
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taatcccagc actttgagag gccaaggcag gtggatcacg aggtcaagag atcgagacca	a 5773
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Met Asp Asp Arg Cys Tyr Pro Val Ile Phe Pro Asp Glu Arg Asn Phe 1 5 10 15 15 Arg Pro Phe Thr Ser Asp Ser Leu Ala Ala Ile Glu Lys Arg Ile Ala	
Met Asp Asp Arg Cys Tyr Pro Val Ile Phe Pro Asp Glu Arg Asn Phe 10 Pro Phe Thr Ser Asp Ser Leu Ala Ala Ile Glu Lys Arg Ile Ala 20 Ile Gln Lys Glu Lys Lys Lys Ser Lys Asp Gln Thr Gly Glu Val Pro	
Met Asp Asp Arg Cys Tyr Pro Val Ile Phe Pro Asp Glu Arg Asn Phe 10 Pro Phe Thr Ser Asp Ser Leu Ala Ala Ile Glu Lys Arg Ile Ala 20 Ile Gln Lys Glu Lys Lys Lys Ser Lys Asp Gln Thr Gly Glu Val Pro 35 Gln Pro Arg Pro Gln Leu Asp Leu Lys Ala Ser Arg Lys Leu Pro Lys	

Lys Arg Thr Ile Tyr Arg Phe Ser Ala Lys His Ala Leu Phe Ile Phe Gly Pro Phe Asn Ser Ile Arg Ser Leu Ala Ile Arg Val Ser Val His Ser Leu Phe Ser Met Phe Ile Ile Gly Thr Val Ile Ile Asn Cys Val Phe Met Ala Thr Gly Pro Ala Lys Asn Ser Asn Ser Asn Asn Thr Asp Ile Ala Glu Cys Val Phe Thr Gly Ile Tyr Ile Phe Glu Ala Leu Ile Lys Ile Leu Ala Arg Gly Phe Ile Leu Asp Glu Phe Ser Phe Leu Arg Asp Pro Trp Asn Trp Leu Asp Ser Ile Val Ile Gly Ile Ala Ile Val Ser Tyr Ile Pro Gly Ile Thr Ile Lys Leu Pro Leu Arg Thr Phe Arg Val Phe Arg Ala Leu Lys Ala Ile Ser Val Val Ser Arg Leu Lys Val Ile Val Gly Ala Leu Leu Arg Ser Val Lys Lys Leu Val Asn Val Ile Ile Leu Thr Phe Phe Cys Leu Ser Ile Phe Ala Leu Val Gly Gln Gln Leu Phe Met Gly Ser Leu Asn Leu Lys Cys Ile Ser Arg Asp Cys Lys Asn Ile Ser Asn Pro Glu Ala Tyr Asp His Cys Phe Glu Lys Lys Glu Asn Ser Pro Glu Phe Lys Met Cys Gly Ile Trp Met Gly Asn Ser Ala Cys Ser Ile Gln Tyr Glu Cys Lys His Thr Lys Ile Asn Pro Asp

325	330	335

Tyr	Asn	Tyr	340	Asn	Phe	Asp	Asn	9he 345	GIY	Trp	ser	Pne	350	Ala	мет
Phe	Arg	Leu 355	Met	Thr	Gln	Asp	Ser 360	Trp	Glu	Lys	Leu	Tyr 365	Gln	Gln	Thr
Leu	Arg 370	Thr	Thr	Gly	Leu	Tyr 375	Ser	Val	Phe	Phe	Phe 380	Ile	Val	Val	Ile
Phe 385	Leu	Gly	Ser	Phe	Tyr 390	Leu	Ile	Asn	Leu	Thr 395	Leu	Ala	Val	Val	Thr
Met	Ala	Tyr	Glu	Glu 405	Gln	Asn	Lys	Asn	Val 410	Ala	Ala	Glu	Ile	Glu 415	Ala
Lys	Glu	Lys	Met 420	Phe	Gln	Glu	Ala	Gln 425	Gln	Leu	Leu	Lys	Glu 430	Glu	Lys
Glu	Ala	Leu 435	Val	Ala	Met	Gly	Ile 440	Asp	Arg	Ser	Ser	Leu 445	Thr	Ser	Leu
Glu	Thr 450	Ser	Tyr	Phe		Pro .455	Lys	Lys	Arg	Lys	Leu 460	Phe	Gly	Asn	Lys
Lys 465	Arg	Lys	Ser	Phe	Phe 470	Leu	Arg	Glu	Ser	Gly 475	Lys	Asp	Gln	Pro	Pro 480
Gly	Ser	Asp	Ser	Asp 485	Glu	Asp	Cys	Gln	Lys 490	Lys	Pro	Gln	Leu	Leu 495	Glu
Gln	Thr	Lys	Arg 500	Leu	Ser	Gln	Asn	Leu 505	Ser	Leu	Asp	His	Phe 510	Asp	Glu
His	Gly	Asp 515	Pro	Leu	Gln	Arg	Gln 520	Arg	Ala	Leu	Ser	Ala 525	Val	Ser	Ile
Leu	Thr 530	Ile	Thr	Met	Lys	Glu 535	Gln	Glu	Lys	Ser	Gln 540	Glu	Pro	Cys	Leu
Pro 545	Cys	Gly	Glu	Asn	Leu 550	Ala	Ser	Lys	Tyr	Leu 555	Val	Trp	Asn	Cys	Cys 560

Pro Gln Trp Leu Cys Val Lys Lys Val Leu Arg Thr Val Met Thr Asp Pro Phe Thr Glu Leu Ala Ile Thr Ile Cys Ile Ile Asn Thr Val Phe Leu Ala Met Glu His His Lys Met Glu Ala Ser Phe Glu Lys Met Leu Asn Ile Gly Asn Leu Val Phe Thr Ser Ile Phe Ile Ala Glu Met Cys Leu Lys Ile Ile Ala Leu Asp Pro Tyr His Tyr Phe Arg Arg Gly Trp Asn Ile Phe Asp Ser Ile Val Ala Leu Leu Ser Phe Ala Asp Val Met Asn Cys Val Leu Gln Lys Arg Ser Trp Pro Phe Leu Arg Ser Phe Arg Val Leu Arg Val Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile Ile Gly Asn Ser Val Gly Ala Leu Gly Ser Leu Thr Val Val Leu Val Ile Val Ile Phe Ile Phe Ser Val Val Gly Met Gln Leu Phe Gly Arg Ser Phe Asn Ser Gln Lys Ser Pro Lys Leu Cys Asn Pro Thr Gly Pro Thr Val Ser Cys Leu Arg His Trp His Met Gly Asp Phe Trp His Ser Phe Leu Val Val Phe Arg Ile Leu Cys Gly Glu Trp Ile Glu Asn Met Trp Glu Cys Met Gln Glu Ala Asn Ala Ser Ser

5er 785	Leu	Cys	Val	Ile	790	Phe	IIe	Leu	Ile	795	Val	11e	GIY	ьуs	800
Val	Val	Leu	Asn	Leu 805	Phe	Ile	Ala	Leu	Leu 810	Leu	Asn	Ser	Phe	Ser 815	Asn
Glu	Glu	Arg	Asn 820	Gly	Asn	Leu	Glu	Gly 825	Glu	Ala	Arg	Lys	Thr 830	Lys	Val
Gln	Leu	Ala 835	Leu	Asp	Arg	Phe	Arg 840	Arg	Ala	Phe	Cys	Phe 845	Val	Arg	His
Thr	Leu 850	Glu	His	Phe	Cys	His 855	Lys	Trp	Cys	Arg	Lys 860	Gln	Asn	Leu	Pro
Gln 865	Gln	Lys	Glu	Val	Ala 870	Gly	Gly	Cys	Ala	Ala 875	Gln	Ser	Lys	Asp	Ile 880
Ile	Pro	Leu	Val	Met 885	Glu	Met	Lys	Arg	Gly 890	Ser	Glu	Thr	Gln	Glu 895	Glu
Leu	Gly	Ile	Leu 900	Thr	Ser	Val	Pro	Lys 905	Thr	Leu	Gly	Val	Arg 910	His	Asp
Trp	Thr	Trp 915	Leu	Ala	Pro	Leu	Ala 920	Glu	Glu	Glu	Asp	Asp 925	Val	Glu	Phe
Ser	Gly 930	Glu	Asp	Asn	Ala	Gln 935	Arg	Ile	Thr	Gln	Pro 940	Glu	Pro	Glu	Gln
Gln 945	Ala	Tyr	Glu	Leu	His 950	Gln	Glu	Asn	Lys	Lys 955	Pro	Thr	Ser	Gln	Arg 960
Val	Gln	Ser	Val	Glu 965	Ile	Asp	Met	Phe	Ser 970	Glu	Asp	Glu	Pro	His 975	Leu
Thr	Ile	Gln	Asp 980	Pro	Arg	Lys	Lys	Ser 985	Asp	Val	Thr	Ser	Ile 990	Leu	Ser
Glu	Cys	Ser 995	Thr	Ile	Asp	Leu	Gln 1000		Gly	y Phe	e Gly	/ Trj		eu Pi	co Glu

Met Val Pro Lys Lys Gln Pro Glu Arg Cys Leu Pro Lys Gly Phe Gly Cys Cys Phe Pro Cys Cys Ser Val Asp Lys Arg Lys Pro Pro Trp Val Ile Trp Trp Asn Leu Arg Lys Thr Cys Tyr Gln Ile Val Lys His Ser Trp Phe Glu Ser Phe Ile Ile Phe Val Ile Leu Leu Ser Ser Gly Ala Leu Ile Phe Glu Asp Val His Leu Glu Asn Gln Pro Lys Ile Gln Glu Leu Leu Asn Cys Thr Asp Ile Ile Phe Thr His Ile Phe Ile Leu Glu Met Val Leu Lys Trp Val Ala Phe Gly Phe Gly Lys Tyr Phe Thr Ser Ala Trp Cys Cys Leu Asp Phe Ile Ile Val Ile Val Ser Val Thr Thr Leu Ile Asn Leu Met Glu Leu Lys Ser Phe Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser Gln Phe Glu Gly Met Lys Val Val Val Asn Ala Leu Ile Gly Ala Ile Pro Ala Ile Leu Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Val Phe Cys Ile Leu Gly Val Tyr Phe Phe Ser Gly Lys Phe Gly Lys Cys Ile Asn Gly Thr Asp Ser Val Ile Asn Tyr Thr Ile Ile Thr Asn Lys Ser Gln Cys Glu Ser Gly Asn Phe Ser Trp

1220	1225	1230

Ile	Asn 1235	Gln	Lys	Val	Asn	Phe 1240	_	Asn	Val	Gly	Asn 1245	Ala	Tyr	Leu
Ala	Leu 1250	Leu	Gln	Val	Ala	Thr 1255	Phe	Lys	Gly	Trp	Met 1260	Asp	Ile	Ile
Tyr	Ala 1265	Ala	Val	Asp	Ser	Thr 1270		Lys	Glu	Gln	Gln 1275	Pro	Glu	Phe
Glu	Ser 1280	Asn	Ser	Leu	Gly	Tyr 1285	Ile	Tyr	Phe	Val	Val 1290	Phe	Ile	Ile
Phe	Gly 1295	Ser	Phe	Phe	Thr	Leu 1300	Asn	Leu	Phe	Ile	Gly 1305	Val	Ile	Ile
Asp	Asn 1310	Phe	Asn	Gln	Gln	Gln 1315	Lys	Lys	Leu	Gly	Gly 1320	Gln	Asp	Ile
Phe	Met 1325	Thr	Glu	Glu	Gln	Lys 1330	Lys	Tyr	Tyr	Asn	Ala 1335	Met	Lys	Lys
Leu	Gly 1340	Ser	Lys	Lys	Pro	Gln 1345	-	Pro	Ile	Pro	Arg 1350	Pro	Leu	Asn
Lys	Cys 1355	Gln	Gly	Leu	Val	Phe 1360	Asp	Ile	Val	Thr	Ser 1365	Gln	Ile	Phe
Asp	Ile 1370	Ile	Ile	Ile	Ser	Leu 1375	Ile	Ile	Leu	Asn	Met 1380	Ile	Ser	Met
Met	Ala 1385	Glu	Ser	Tyr	Asn	Gln 1390	Pro	Lys	Ala	Met	Lys 1395		Ile	Leu
Asp	His 1400	Leu	Asn	Trp	Val	Phe 1405	Val	Val	Ile	Phe	Thr 1410	Leu	Glu	Cys
Leu	Ile 1415	Lys	Ile	Phe	Ala	Leu 1420	Arg	Gln	Tyr	Tyr	Phe 1425		Asn	Gly
Trp	Asn 1430	Leu	Phe	Asp	Cys	Val 1435	Val	Val	Leu	Leu	Ser 1440	Ile	Val	Ser

Thr Met Ile Ser Thr Leu Glu Asn Gln Glu His Ile Pro Phe Pro Pro Thr Leu Phe Arg Ile Val Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Val Arg Ala Ala Arg Gly Ile Arg Thr Leu Leu Phe Ala Leu Met Met Ser Leu Pro Ser Leu Phe Asn Ile Gly Leu Leu Leu Phe Leu Ile Met Phe Ile Tyr Ala Ile Leu Gly Met Asn Trp Phe Ser Lys Val Asn Pro Glu Ser Gly Ile Asp Asp Ile Phe Asn Phe Lys Thr Phe Ala Ser Ser Met Leu Cys Leu Phe Gln Ile Ser Thr Ser Ala Gly Trp Asp Ser Leu Leu Ser Pro Met Leu Arg Ser Lys Glu Ser Cys Asn Ser Ser Ser Glu Asn Cys His Leu Pro Gly Ile Ala Thr Ser Tyr Phe Val Ser Tyr Ile Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu Glu Asn Phe Asn Thr Ala Thr Glu Glu Ser Glu Asp Pro Leu Gly Glu Asp Asp Phe Asp Ile Phe Tyr Glu Val Trp Glu Lys Phe Asp Pro Glu Ala Thr 1625 1630 1635

Gln Phe Ile Lys Tyr Ser Ala Leu Ser Asp Phe Ala Asp Ala Leu

Pro	Glu 1655	Pro	Leu	Arg	Val	Ala 1660	Lys	Pro	Asn	Lys	Tyr 1665	Gln	Phe	Leu		
Val	Met 1670	Asp	Leu	Pro	Met	Val 1675	Ser	Glu	Asp	Arg	Leu 1680	His	Cys	Met		
Asp	Ile 1685	Leu	Phe	Ala	Phe	Thr 1690	Ala	Arg	Val	Leu	Gly 1695	Gly	Ser	Asp		
Gly	Leu 1700	Asp	Ser	Met	Lys	Ala 1705		Met	Glu	Glu	Lys 1710	Phe	Met	Glu		
Ala	Asn 1715	Pro	Leu	Lys	Lys	Leu 1720		Glu	Pro	Ile	Val 1725	Thr	Thr	Thr		
Lys	Arg 1730	Lys	Glu	Glu	Glu	Arg 1735	Gly	Ala	Ala	Ile	Ile 1740	Gln	Lys	Ala		
Phe	Arg 1745	Lys	Tyr	Met	Met	Lys 1750	Val	Thr	Lys	Gly	Asp 1755	Gln	Gly	Asp		
Gln	Asn 1760	Asp	Leu	Glu	Asn	Gly 1765	Pro	His	Ser	Pro	Leu 1770	Gln	Thr	Leu		
Cys	Asn 1775	-	Asp	Leu	Ser	Ser 1780		Gly	Val	Ala	Lys 1785		Lys	Val		
His	Cys 1790	Asp														
	0> 5)(5		1>	5822	<21	2 > D1	NA <	213>	Mu	s mu	sculu	s <2	220>	<221>	CDS	<222>
			mi	sc_f	eatu	re <2	22>	(58	04).	. (58	04) <	223>	n :	= a or	t or	c or g
	00> ! gagcc		ggtg		atg (Met (gag g Glu G	ag a	gg t rg T 5	ac t yr T	at c yr P	ca gte ro Va	g ato	e tto Pho 10	c cca e Pro		51
		Arg i				ccc to Pro P		hr P								99
						caa a								c aag	:	147

30 35 40

_	_				cag Gln				_		_				195
					ctc Leu 65										243
					ctg Leu										291
_	_	_		_	aag Lys	_				_		_	_	_	339
					ggg Gly										387
					tca Ser										435
					ttc Phe 145										483
					ccc Pro										531
_	_				ata Ile	_	_	_				 _			579
					cct Pro										627
					tgt Cys										675
					cga Arg 225										723
			_	_	gtc Val				_	_					771
					atg Met										819

_	_	gtt Val 270		_	_			_			_	_	_		_	867
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cgg aag tat ttc a Arg Lys Tyr Phe 1 1095		tgc tgg ctc gat Cys Trp Leu Asp 1105	
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						cgc Arg 1445									4377
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	agg Arg 1710														5187
	cgg Arg 1725														5232
	tca Ser 1740					cag Gln 1745									5277
	ttg Leu 1755					atc Ile 1760						tgaa	acco	ccc	5323
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Ile	Gln	Lys 35	Glu	Lys	Lys	Lys	Ser 40	Lys	Asp	Lys	Ala	Ala 45	Thr	Glu	Pro
Gln	Pro 50	Arg	Pro	Gln	Leu	Asp 55	Leu	Lys	Ala	Ser	Arg 60	Lys	Leu	Pro	Lys
Leu 65	Tyr	Gly	Asp	Val	Pro 70	Pro	Asp	Leu	Ile	Ala 75	Lys	Pro	Leu	Glu	Asp 80
Leu	Asp	Pro	Phe	Tyr 85	Lys	Asp	His	Lys	Thr 90	Phe	Met	Val	Leu	Asn 95	Lys
Lys	Arg	Thr	Ile 100	Tyr	Arg	Phe	Ser	Ala 105	Lys	Arg	Ala	Leu	Phe 110	Ile	Leu
Gly	Pro	Phe 115	Asn	Pro	Ile	Arg	Ser 120	Phe	Met	Ile	Arg	Ile 125	Ser	Val	His
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Phe 145	Met	Ala	Asn	Asn	Ser 150	Ser	Val	Asp	Ser	Arg 155	Pro	Ser	Ser	Asn	Ile 160
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Cys	Phe 210	Leu	Gly	Asn	Lys	Val 215	Asn	Asn	Leu	Ser	Thr 220	Leu	Arg	Thr	Phe
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Tyr Glu Glu Gln Asn Arq Asn Val Ala Ala Glu Thr Glu Ala Lys Glu Lys Met Phe Gln Glu Ala Gln Gln Leu Leu Arg Glu Glu Lys Glu Ala Leu Val Ala Met Gly Ile Asp Arg Thr Ser Leu Asn Ser Leu Gln Ala Ser Ser Phe Ser Pro Lys Lys Arg Lys Phe Phe Gly Ser Lys Thr Arg Lys Ser Phe Phe Met Arg Gly Ser Lys Thr Ala Arg Ala Ser Ala Ser Asp Ser Glu Asp Asp Ala Ser Lys Asn Pro Gln Leu Leu Glu Gln Thr Lys Arg Leu Ser Gln Asn Leu Pro Val Glu Leu Phe Asp Glu His Val Asp Pro Leu His Arg Gln Arg Ala Leu Ser Ala Val Ser Ile Leu Thr Ile Thr Met Gln Glu Gln Glu Lys Ser Gln Glu Pro Cys Phe Pro Cys Gly Lys Asn Leu Ala Ser Lys Tyr Leu Val Trp Glu Cys Ser Pro Pro Trp Leu Cys Ile Lys Lys Val Leu Gln Thr Ile Met Thr Asp Pro Phe Thr Glu Leu Ala Ile Thr Ile Cys Ile Ile Val Asn Thr Val Phe Leu Ala Met Glu His His Asn Met Asp Asn Ser Leu Lys Asp Ile Leu Lys Ile Gly Asn Trp Val Phe Thr Gly Ile Phe Ile Ala Glu Met Cys Leu

Lys Ile Ile Ala Leu Asp Pro Tyr His Tyr Phe Arg His Gly Trp Asn

Ile	Phe	Asp	Ser	Ile	Val	Ala	Leu	Val	Ser	Leu	Ala	Asp	Val	Leu	Phe
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Ser Arg Asp Thr Ala Thr Leu Asp Thr Arg Ser Trp Lys Glu Tyr Asp

Leu Lys Cys Thr Asp Asn Ile Phe Thr Phe Ile Phe Leu Leu Glu

Ser Ala Trp Cys Trp Leu Asp Phe Leu Ile Val Val Ser Val Leu Ser Leu Thr Asn Leu Pro Asn Leu Lys Ser Phe Arg Asn Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser Gln Phe Glu Gly Met Lys Val Val Val Asn Ala Leu Met Ser Ala Ile Pro Ala Ile Leu Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile Phe Cys Ile Leu Gly Val Asn Phe Phe Ser Gly Lys Phe Gly Arg Cys Ile Asn Gly Thr Asp Ile Asn Lys Tyr Phe Asn Ala Ser Asn Val Pro Asn Gln Ser Gln Cys Leu Val Ser Asn Tyr Thr Trp Lys Val Pro Asn Val Asn Phe Asp Asn Val Gly Asn Ala Tyr Leu Ala Leu Leu Gln Val Ala Thr Tyr Lys Gly Trp Leu Asp Ile Met Asn Ala Ala Val

Asp Ser Arg Gly Lys Asp Glu Gln Pro Ala Phe Glu Ala Asn Leu

Tyr Ala Tyr Leu Tyr Phe Val Val Phe Ile Ile Phe Gly Ser Phe

Phe Thr Leu Asn Leu Phe Ile Gly Val Ile Ile Asp Asn Phe Asn

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- Phe Val Phe Asp Leu Val Thr Ser Gln Val Phe Asp Val Ile Ile 1340 1345 1350
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- Asp Cys Val Val Val Val Leu Ser Ile Ile Ser Thr Leu Val Ser 1415 · 1420 1425
- Gly Leu Glu Asn Ser Asn Val Phe Pro Pro Thr Leu Phe Arg Ile 1430 1435 1440
- Val Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Val Arg Ala 1445 1450 1455
- Ala Arg Gly Ile Arg Thr Leu Leu Phe Ala Leu Met Met Ser Leu 1460 1465 1470
- Pro Ser Leu Phe Asn Ile Gly Leu Leu Phe Leu Val Met Phe 1475 1480 1485
- Ile Tyr Ala Ile Phe Gly Met Asn Trp Phe Ser Lys Val Lys Arg 1490 1495 1500
- Gly Ser Gly Ile Asp Asp Ile Phe Asn Phe Asp Thr Phe Ser Gly

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Tyr	Ile 1580	Ala	Val	Ile	Leu	Glu 1585	Asn	Phe	Asn	Thr	Ala 1590	Thr	Glu	Glu
Ser	Glu 1595	Asp	Pro	Leu		Glu 1600	Asp	Asp	Phe	Glu	Ile 1605	Phe	Tyr	Glu
Ile	Trp 1610	Glu	Lys	Phe	Asp	Pro 1615	Glu	Ala	Thr	Gln	Phe 1620	Ile	Gln	Tyr
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Val	Ala 1640	_	Pro	Asn	Arg	Phe 1645		Phe	Leu	Met	Met 1650	Asp	Leu	Pro
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<220> <221> misc_feature <223> Reverse strand of SalI linker with NotI/XbaI

overhangs

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T>C at nt 4056

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				gtc Val							624

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													ata Ile			1824
													aag Lys			1872
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					ccg Pro 870											26	540
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				885					090					095		
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gag acc aag ca Glu Thr Lys G 930	ln Leu Thr		sp Asp Gln (
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aag tot gac go Lys Ser Asp A					sp Leu
aat gat atc to Asn Asp Ile Pl 90			ys Thr Val S		
cca gat aga to Pro Asp Arg Cy 995					tgc cac 3024 Cys His
_	aag aga aag Lys Arg Lys		tgg gtc ctc Trp Val Let	g tgg tgg aac u Trp Trp Asr 1020	
			aag cac ago Lys His Sen	c tgg ttt gag r.Trp Phe Glu 1035	
	ttt gtt att Phe Val Ile		agc agt gga Ser Ser Gly	a gcg ctg ata y Ala Leu Ile 1050	_
gaa gat gtc a Glu Asp Val A 1055			_		
agg tgt acc		ttc aca	ttt att tto	c ctc ctc cas	atg 3249
				e Leu Leu Glu 1080	
Arg Cys Thr 1	Asp Asn Ile	Phe Thr 1075 ttt gga	Phe Ile Phe	e Leu Leu Glu 1080 g tat ttc acc	: agt 3294

agt Ser	ctc Leu 1115	atg Met	aat Asn	cta Leu	cca Pro	agc Ser 1120	ttg Leu	aag Lys	tcc Ser	ttc Phe	cgg Arg 1125	act Thr	ctg Leu	cgg Arg	3	384
											gaa Glu 1140				3	429
_	_	_		_	_		_	_			gcc Ala 1155				3	474
											ttt Phe 1170				3	519
											tgc Cys 1185				3	564
											gtt Val 1200				3	609
											gtc Val 1215				3	654
											ctg Leu 1230				3	699
_	acc Thr 1235										gct Ala 1245				3	744
											gcg Ala 1260				3	789
											ggc Gly 1275				3	834
											aac Asn 1290				3	879
											atg Met 1305		gaa Glu		3	924
_											gga Gly 1320				3	969

						agg Arg 1330									4014
						agc Ser 1345							atc Ile		4059
						atg Met 1360									4104
_	cag Gln 1370	ccc Pro	aaa Lys	gat Asp	gtg Val	aag Lys 1375	aaa Lys	acc Thr	ttt Phe	gat Asp	atc Ile 1380	ctc Leu	aac Asn	ata Ile	4149
_	ttc Phe 1385					acc Thr 1390									4194
						ttc Phe 1405									4239
						tct Ser 1420									4284
						tct Ser 1435									4329
_	cgc Arg 1445					ggt Gly 1450									4374
_						ctc Leu 1465									4419
						ggt Gly 1480	_	_			_		_		4464
						atg Met 1495									4509
						atc Ile 1510									4554
_	atg Met 1520					cag Gln 1525									4599
acc	ctc	ctc	aac	ccc	atg	ctg	gag	gca	aaa	gaa	cac	tgc	aac	tcc	4644

Thr	Leu 1535	Leu	Asn	Pro	Met	Leu 1540	Glu	Ala	Lys	Glu	His 1545	Cys	Asn	Ser		
	tcc Ser 1550										gcc Ala 1560					4689
	gtc Val 1565										gtg Val 1575					4734
											gcc Ala 1590					4779
											atc Ile 1605					4824
	tgg Trp 1610										ttc Phe 1620					4869
_	gcc Ala 1625										gag Glu 1635					4914
		Lys									atg Met 1650					4959
_	gtg Val 1655										gtt Val 1665					5004
	act Thr 1670										ttg Leu 1680					5049
	acc Thr 1685	atg Met	atg Met	gag Glu	gag Glu	aag Lys 1690	ttt Phe	atg Met	gag Glu	gcc Ala	aac Asn 1695	cct Pro	ttt Phe	aag Lys		5094
_	ctc Leu 1700	Tyr									agg Arg 1710					5139
-	caa Gln 1715	ggc Gly	gcc Ala	gcc Ala	gtc Val	atc Ile 1720	cag Gln	agg Arg	gcc Ala	tac Tyr	cgg Arg 1725	aaa Lys	cac His	atg Met		5184
	aag Lys 1730	Met	gtc Val	aaa Lys	ctg Leu	agg Arg 1735	ctg Leu	aag Lys	gac Asp	agg Arg	tca Ser 1740	agt Ser	tca Ser		•	5229
	cag Gln										ttg Leu					5274

aag gtc aag gtt cac aat gac tga

Lys Val Lys Val His Asn Asp

<210> 20 <211> 1765 <212> PRT <213> Rattus norvegicus <400> 20

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Arg Pro Phe Thr Ser Asp Ser Leu Ala Ala Ile Glu Lys Arg Ile Ala

Ile Gln Lys Glu Arg Lys Lys Ser Lys Asp Lys Ala Ala Ala Glu Pro

Gln Pro Arg Pro Gln Leu Asp Leu Lys Ala Ser Arg Lys Leu Pro Lys

Leu Tyr Gly Asp Ile Pro Pro Glu Leu Val Ala Lys Pro Leu Glu Asp

Leu Asp Pro Phe Tyr Lys Asp His Lys Thr Phe Met Val Leu Asn Lys

Lys Arg Thr Ile Tyr Arg Phe Ser Ala Lys Arg Ala Leu Phe Ile Leu

Gly Pro Phe Asn Pro Leu Arg Ser Leu Met Ile Arg Ile Ser Val His

Ser Val Phe Ser Met Phe Ile Ile Cys Thr Val Ile Ile Asn Cys Met

Phe Met Ala Asn Ser Met Glu Arg Ser Phe Asp Asn Asp Ile Pro Glu

Tyr Val Phe Ile Gly Ile Tyr Ile Leu Glu Ala Val Ile Lys Ile Leu

Ala Arg Gly Phe Ile Val Asp Glu Phe Ser Phe Leu Arg Asp Pro Trp

Asn Trp Leu 1	Asp Phe	Ile Val	Ile (Gly Th	nr Ala	Ile	Ala 205	Thr	Cys	Phe
Pro Gly Ser (Gln Val	Asn Leu 215		Ala Le	eu Arg	Thr 220	Phe	Arg	Val	Phe
Arg Ala Leu 1 225	Lys Ala	Ile Ser 230	Val :	Ile Se	er Gly 235	Leu	Lys	Val	Ile	Val 240
Gly Ala Leu 1	Leu Arg 245	Ser Val	Lys :	Lys Le 25		Asp	Val	Met	Val 255	Leu
Thr Leu Phe (Cys Leu 260	Ser Ile		Ala Le 265	eu Val	Gly	Gln	Gln 270	Leu	Phe
Met Gly Ile 1 275	Leu Asn	Gln Lys	Cys :	Ile Ly	s His	Asn	Cys 285	Gly	Pro	Asn
Pro Ala Ser A	Asn Lys	Asp Cys 295		Glu Ly	⁄s Glu	Lys 300	Asp	Ser	Glu	Asp
Phe Ile Met 0	Cys Gly	Thr Trp	Leu (Gly Se	er Arg 315	Pro	Cys	Pro	Asn	Gly 320
Ser Thr Cys i	Asp Lys 325	Thr Thr	Leu /	Asn Pr 33		Asn	Asn	Tyr	Thr 335	Lys
Phe Asp Asn 1	Phe Gly 340	Trp Ser		Leu Al 345	la Met	Phe	Arg	Val 350	Mėt	Thr
Gln Asp Ser 3	Trp Glu	Arg Leu	Tyr 2	Arg Gl	ln Ile	Leu	Arg 365	Thr	Ser	Gly
Ile Tyr Phe V	Val Phe	Phe Phe		Val Va	al Ile	Phe 380	Leu	Gly	Ser	Phe
Tyr Leu Leu 1 385	Asn Leu	Thr Leu	Ala	Val Va	al Thr 395	Met	Ala	Tyr	Glu	Glu 400
Gln Asn Arg i	Asn Val 405	Ala Ala	Glu '	Thr Gl 41		Lys	Glu	Lys	Met 415	Phe
Gln Glu Ala (Gln Gln	Leu Leu	Arg	Glu Gl	lu Lys	Glu	Ala	Leu	Val	Ala

420	425	430

Met	Gly	Ile 435	Asp	Arg	Ser	Ser	Leu 440	Asn	Ser	Leu	Gln	Ala 445	Ser	Ser	Phe
Ser	Pro 450	Lys	Lys	Arg	Lys	Phe 455	Phe	Gly	Ser	Lys	Thr 460	Arg	Lys	Ser	Phe
Phe 465	Met	Arg	Gly	Ser	Lys 470	Thr	Ala	Gln	Ala	Ser 475	Ala	Ser	Asp	Ser	Glu 480
Asp	Asp	Ala	Ser	Lys 485	Asn	Pro	Gln	Leu	Leu 490	Glu	Gln	Thr	Lys	Arg 495	Leu
Ser	Gln	Asn	Leu 500	Pro	Val	Asp	Leu	Phe 505	Asp	Glu	His	Val	Asp 510	Pro	Leu
His	Arg	Gln 515	Arg	Ala	Leu	Ser	Ala 520	Val	Ser	Ile	Leu	Thr 525	Ile	Thr	Met
Gln	Glu 530	Gln	Glu	Lys	Phe	Gln 535	Glu	Pro	Cys	Phe	Pro 540	Cys	Gly	Lys	Asn
Leu 545	Ala	Ser	Lys	Tyr	Leu 550	Val	Trp	Asp	Cys	Ser 555	Pro	Gln	Trp	Leu	Cys 560
Ile	Lys	Lys	Val	Leu 565	Arg	Thr	Ile	Met	Thr 570	Asp	Pro	Phe	Thr	Glu 575	Leu
Ala	Ile	Thr	Ile 580	Cys	Ile	Ile	Ile	Asn 585	Thr	Val	Phe	Leu	Ala 590	Val	Glu
His	His	Asn 595	Met	Asp	Asp	Asn	Leu 600	Lys	Thr	Ile	Leu	Lys 605	Ile	Gly	Asn
Trp	Val 610	Phe	Thr	Gly	Ile	Phe 615	Ile	Ala	Glu	Met	Cys 620	Leu	Lys	Ile	Ile
Ala 625	Leu	Asp	Pro	Tyr	His 630	Tyr	Phe	Arg	His	Gly 635	Trp	Asn	Val	Phe	Asp 640

Ser Ile Val Ala Leu Leu Ser Leu Ala Asp Val Leu Tyr Asn Thr Leu 645 650 655

Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile Ile Gly His Ser Val Gly Ala Leu Gly Asn Leu Thr Val Val Leu Thr Ile Val Val Phe Ile Phe Ser Val Val Gly Met Arg Leu Phe Gly Thr Lys Phe Asn Lys Thr Ala Tyr Ala Thr Gln Glu Arg Pro Arg Arg Trp His Met Asp Asn Phe Tyr His Ser Phe Leu Val Val Phe Arg Ile Leu Cys Gly Glu Trp Ile Glu Asn Met Trp Gly Cys Met Gln Asp Met Asp Gly Ser Pro Leu Cys Ile Ile Val Phe Val Leu Ile Met Val Ile Gly Lys Leu Val Val Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser Phe Ser Asn Glu Glu Lys Asp Gly Ser Leu Glu Gly Glu Thr Arg Lys Thr Lys Val Gln Leu Ala Leu Asp Arg Phe Arg Arg Ala Phe Ser Phe Met Leu His Ala Leu Gln Ser Phe Cys Cys Lys Lys Cys Arg Arg Lys Asn Ser Pro Lys Pro Lys Glu Thr Thr Glu Ser Phe Ala Gly Glu Asn Lys Asp Ser Ile Leu Pro Asp Ala Arg Pro Trp Lys Glu Tyr Asp Thr

Ser Asp Asn Asn Arg Ser Phe Leu Ala Ser Leu Arg Val Leu Arg Val

- Asp Met Ala Leu Tyr Thr Gly Gln Ala Gly Ala Pro Leu Ala Pro Leu 885 890 895
- Ala Glu Val Glu Asp Asp Val Glu Tyr Cys Gly Glu Gly Gly Ala Leu 900 905 910
- Pro Thr Ser Gln His Ser Ala Gly Val Gln Ala Gly Asp Leu Pro Pro 915 920 925
- Glu Thr Lys Gln Leu Thr Ser Pro Asp Asp Gln Gly Val Glu Met Glu 930 935 940
- Val Phe Ser Glu Glu Asp Leu His Leu Ser Ile Gln Ser Pro Arg Lys 945 950 955 960
- Lys Ser Asp Ala Val Ser Met Leu Ser Glu Cys Ser Thr Ile Asp Leu 965 970 975
- Asn Asp Ile Phe Arg Asn Leu Gln Lys Thr Val Ser Pro Lys Lys Gln 980 985 990
- Pro Asp Arg Cys Phe Pro Lys Gly Leu Ser Cys His Phe Leu Cys His 995 1000 1005
- Lys Thr Asp Lys Arg Lys Ser Pro Trp Val Leu Trp Trp Asn Ile 1010 1015 1020
- Arg Lys Thr Cys Tyr Gln Ile Val Lys His Ser Trp Phe Glu Ser 1025 1030 1035
- Phe Ile Ile Phe Val Ile Leu Leu Ser Ser Gly Ala Leu Ile Phe 1040 1045 1050
- Glu Asp Val Asn Leu Pro Ser Arg Pro Gln Val Glu Lys Leu Leu 1055 1060 1065
- Arg Cys Thr Asp Asn Ile Phe Thr Phe Ile Phe Leu Leu Glu Met 1070 1075 1080
- Ile Leu Lys Trp Val Ala Phe Gly Phe Arg Arg Tyr Phe Thr Ser 1085 1090 1095

- Ala Trp Cys Trp Leu Asp Phe Leu Ile Val Val Val Ser Val Leu Ser Leu Met Asn Leu Pro Ser Leu Lys Ser Phe Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser Gln Phe Glu Gly Met Lys Val Val Val Tyr Ala Leu Ile Ser Ala Ile Pro Ala Ile Leu Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Val Phe Cys Ile Leu Gly Val Asn Leu Phe Ser Gly Lys Phe Gly Arg Cys Ile Asn Gly Thr Asp Ile Asn Met Tyr Leu Asp Phe Thr Glu Val Pro Asn Arg Ser Gln Cys Asn Ile Ser Asn Tyr Ser Trp Lys Val Pro Gln Val Asn Phe Asp Asn Val Gly Asn Ala Tyr Leu Ala Leu Leu Gln Val Ala Thr Tyr Lys Gly Trp Leu Glu Ile Met Asn Ala Ala Val Asp Ser Arg Glu Lys Asp Glu Gln Pro Asp Phe Glu Ala Asn Leu Tyr Ala Tyr Leu Tyr Phe Val Val Phe Ile Ile Phe Gly Ser Phe Phe Thr Leu Asn Leu Phe Ile Gly Val Ile Ile Asp Asn Phe Asn Gln
- Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys Leu Gly Thr Lys Lys

Gln Gln Lys Lys Leu Gly Gly Gln Asp Ile Phe Met Thr Glu Glu

1310	1315	1320

Pro	Gln 1325	_	Pro	Ile	Pro	Arg 1330	Pro	Leu	Asn	Lys	Cys 1335		Ala	Phe
Val	Phe 1340	Asp	Leu	Val	Thr	Ser 1345	Gln	Val	Phe	Asp	Val 1350	Ile	Ile	Leu
Gly	Leu 1355		Val	Leu	Asn	Met 1360		Ile	Met	Met	Ala 1365		Ser	Ala
Asp	Gln 1370	Pro	Lys	Asp	Val	Lys 1375	Lys	Thr	Phe	Asp	Ile 1380	Leu	Asn	Ile
Ala	Phe 1385	Val	Val	Ile	Phe	Thr 1390	Ile	Glu	Cys	Leu	Ile 1395	Lys	Val	Phe
Ala	Leu 1400	Arg	Gln	His	Tyr	Phe 1405	Thr	Asn	Gly	Trp	Asn 1410	Leu	Phe	Asp
Cys	Val 1415	Val	Val	Val	Leu	Ser 1420	Ile	Ile	Ser	Thr	Leu 1425	Val	Ser	Arg
Leu	Glu 1430	_	Ser	Asp	Ile	Ser 1435		Pro	Pro	Thr	Leu 1440		Arg	Val
Val	Arg 1445	Leu	Ala	Arg	Ile	Gly 1450	Arg	Ile	Leu	Arg	Leu 1455	Val	Arg	Ala
Ala	Arg 1460	Gly	Ile	Arg	Thr	Leu 1465	Leu	Phe	Ala	Leu	Met 1470	Met	Ser	Leu
Pro	Ser 1475	Leu	Phe	Asn	Ile	Gly 1480	Leu	Leu	Leu	Phe	Leu 1485	Val	Met	Phe
Ile	Tyr 1490	Ala	Ile	Phe	Gly	Met 1495	Ser	Trp	Phe	Ser	Lys 1500	Val	Lys	Lys
Gly	Ser 1505	Gly	Ile	Asp	Asp	Ile 1510	Phe	Asn	Phe	Glu	Thr 1515	Phe	Thr	Gly
Ser	Met 1520	Leu	Cys	Leu	Phe	Gln 1525	Ile	Thr	Thr	Ser	Ala 1530	Gly	Trp	Asp

Thr Leu Leu Asn Pro Met Leu Glu Ala Lys Glu His Cys Asn Ser Ser Ser Gln Asp Ser Cys Gln Gln Pro Gln Ile Ala Val Val Tyr Phe Val Ser Tyr Ile Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu Glu Asn Phe Asn Thr Ala Thr Glu Glu Ser Glu Asp Pro Leu Gly Glu Asp Asp Phe Glu Ile Phe Tyr Glu Val Trp Glu Lys Phe Asp Pro Glu Ala Ser Gln Phe Ile Gln Tyr Ser Ala Leu Ser Asp Phe Ala Asp Ala Leu Pro Glu Pro Leu Arg 1630 1635 Val Ala Lys Pro Asn Lys Phe Gln Phe Leu Val Met Asp Leu Pro Met Val Met Gly Asp Arg Leu His Cys Met Asp Val Leu Phe Ala Phe Thr Thr Arg Val Leu Gly Asp Ser Ser Gly Leu Asp Thr Met Lys Thr Met Met Glu Glu Lys Phe Met Glu Ala Asn Pro Phe Lys Lys Leu Tyr Glu Pro Ile Val Thr Thr Thr Lys Arg Lys Glu Glu Glu Gln Gly Ala Ala Val Ile Gln Arg Ala Tyr Arg Lys His Met 1720 1725 Glu Lys Met Val Lys Leu Arg Leu Lys Asp Arg Ser Ser Ser

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His Gln Val Phe Cys Asn Gly Asp Leu Ser Ser Leu Asp Val Ala
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                                            1755
Lys Val Lys Val His Asn Asp
    1760
                        1765
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<2:12> PRT
<213> Rattus norvegicus
<400> 21
Ile Asp His His His His His
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<210> 22
<211> 16
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Peptide for
      raising antibodies
<400> 22
Cys Asn Gly Asp Leu Ser Ser Phe Gly Val Ala Lys Gly Lys Val His
                5
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<211> 18
<212> PRT
<213> Artificial Sequence
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Cys Asn Asp Gly Leu Ser Ser Leu Asp Val Ala Lys Val Lys Val His
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Asn Asp
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<210> 25
<211> 30
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: PCR primer
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ggttctagat cagtcacagt ggaccttgcc
<210> 26
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: PCR primer
<400> 26
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gcctcggcga aagtagtggt agg
<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: PCR primer
<400> 27
                                                                 22
cctaccacta ctttcgccga gg
<210> 28
<211> 24
<212> DNA
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<223> Description of Artificial Sequence: PCR primer
<400> 28
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tacgaagtaa atgtaaccga gtga
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<213> Artificial Sequence
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gccatggaac accacaatat g
<210> 33
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